

RESULT 1

AAB51244

ID AAB51244 standard; protein; 662 AA.

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AC AAB51244;

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DT 26-MAR-2001 (first entry)

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DE Human haemopoietin receptor protein NR10.3 SEQ ID NO:17.

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KW Human; haemopoietin receptor; NR10.1; NR10.2; NR10.3; NR10;

KW immunoregulation; haematopoietic cell regulation; transmembrane;

KW immune disorder; haematopoietic disorder; autoimmune disease; allergy;

KW metal allergy; pollen allergy.

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OS Homo sapiens.

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PN WO200075314-A1.

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PD 14-DEC-2000.

XX

PF 01-JUN-2000; 2000WO-JP003556.

XX

PR 02-JUN-1999; 99JP-00155797.

PR 30-JUL-1999; 99JP-00217797.

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PA (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.

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PI Maeda M, Yaguchi N;

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DR WPI; 2001-061720/07.

DR N-PSDB; AAC92350.

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PT Hematopoietin receptor protein NR10 for screening potential ligands for

PT treatment of immune and hematopoietic disorders such as autoimmune

PT diseases and allergies.

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PS Claim 1; Fig 13-14; 127pp; Japanese.

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CC The present sequence represents a human haemopoietin receptor protein

CC (NR10), specifically designated NR10.3. NR10 occurs as a transmembrane

CC protein and a soluble protein. NR10 is a haemopoietin receptor molecule

CC which participates in immunoregulation and haematopoietic cell regulation

CC in vivo, and is useful in searching for haematopoietic factors capable of

CC binding to the receptor. NR10 can be used for the identification of

CC substances for the treatment and prevention of immune and haematopoietic

CC disorders including autoimmune diseases and allergies such as metal and

CC pollen allergy

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SQ Sequence 662 AA;

Query Match 100.0%; Score 3528; DB 4; Length 662;
 Best Local Similarity 100.0%; Pred. No. 6.5e-291;
 Matches 662; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKLSPQPSCVNLGMMWTWALWMLPSLCKFSLAALPAKPENISCVYYRKNLTCTWSPGKE 60

Db 1 MKLSPQPSCVNLGMMWTWALWMLPSLCKFSLAALPAKPENISCVYYRKNLTCTWSPGKE 60

Qy 61 TSYTQYTVKRTYAFGEKHDNCTNSSTSENASCSSFFLPRITIPDNYTIEVEAENG DGVI 120

Db 61 TSYTQYTVKRTYAFGEKHDNCTNSSTSENASCSSFFLPRITIPDNYTIEVEAENG DGVI 120

Qy 121 KSHMTYWRLENIakteppkIFRVKPVLGIKRMIQIEWIKPELAPVSSDLKYTLRFRTVNS 180

Db 121 KSHMTYWRLENIakteppkIFRVKPVLGIKRMIQIEWIKPELAPVSSDLKYTLRFRTVNS 180

Qy 181 TSWMEVNFakNRKDKNQTYNLTGLQPFTEYVIALRCavKESKFWSDSQEKMGMTTEEAP 240

Db 181 TSWMEVNFakNRKDKNQTYNLTGLQPFTEYVIALRCavKESKFWSDSQEKMGMTTEEAP 240

Qy 241 CGLELWRVLKPAEADGRRPVRLLWKKARGAPVLEKTLGYNiWYYPESNTNLTETMNTNQ 300

Db 241 CGLELWRVLKPAEADGRRPVRLLWKKARGAPVLEKTLGYNiWYYPESNTNLTETMNTNQ 300

Qy 301 QLELHLGGESFWVSMISYNSLGKSPVATLRIPAIQEKSFQCIEMQACVAEDQLVVKWQS 360

Db 301 QLELHLGGESFWVSMISYNSLGKSPVATLRIPAIQEKSFQCIEMQACVAEDQLVVKWQS 360

Sequence Query
 Appendix A

